



CCACGGTCCGGTCAGTCTGGTTCGGAGAACGAGCGGTGGCGTGGGCCATCCGGGGAATGGGC
GCCCTCGTGACCTAGTGTGCGGGGCAAAAGGTCTTGCCGGCCCTCGCTCGTCAGGGCGGTAT
CTGGCGCCTGAGCGGGCGTGGAGCCCTTGGAGCCCGCAGCAGGGGCACACCCGGAAACCG
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CAAACTCGCCGACCTGCGCTACCTGAGCGCGCGCTCTGGCACTGTGTCTCGCCCGCCACG
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CTTGAAGACTCAGAAATATCTTATTGGACAATGAATTTCAATGTTAAGATTGCAGATTTTGGTTTAT
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CTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAA
ATGGGTCTTCAGCCTTACCGGAAATACCTGTGTTTCTAGATCACCATCTTTAAATTTACTTCA
AAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTGTTTTCATAAAGGATATTTATAAA
AAAAA

(SEQ ID NO: 1)

FIG. 1



NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Val Thr Ile Ser Pro Tyr His Lys Leu Ala Asp 20
Leu Arg Val Gln Val Leu Ser Arg Glu Val Arg Glu His Thr Ser Ser Ala Arg Arg Trp 40
Arg Val Gln Val Leu Ser Arg Glu Val Arg Glu His Thr Ser Ser Ala Arg Arg Trp 60
Lys Asp Val Leu Arg Glu Val Arg Glu His Thr Ser Ser Ala Arg Arg Trp 80
Ile Leu Gly Ile Cys Asn Glu Leu His Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 100
Gly Ser Leu Asn Glu Leu His Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 120
Arg Phe Arg Ile Leu His Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 140
Pro Leu Leu His Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 160
Lys Ile Ala Asp Phe Glu Leu His Thr Ser Ser Ala Arg Arg Trp 180
Ser Lys Ser Ala Pro Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 200
Gly Gln Lys Ser Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 220
Glu Val Leu Ser Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 240
Ser Val Ser Gln Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 260
His Arg Ala Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 280
Pro Ser Phe Leu Cys Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 300
Ile His Leu Cys Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 320
Pro Gln Glu Ser Leu Cys Asp Glu Leu His Thr Ser Ser Ala Arg Arg Trp 340
Ser Arg Ser Leu Pro Leu His Thr Ser Ser Ala Arg Arg Trp 360
Tyr Phe Met Lys Leu Pro Leu His Thr Ser Ser Ala Arg Arg Trp 380
Ser Gln Arg Ala Ala Phe Glu Leu His Thr Ser Ser Ala Arg Arg Trp 400
Pro Leu Ser Thr Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 420
Gln Ser Lys Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 440
Asp Ala Leu Ser Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 460
Pro Thr Arg Thr Ser Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 480
Phe Ala Lys Val Ile Val Gln Lys Leu His Thr Ser Ser Ala Arg Arg Trp 500
Pro Glu Ile Leu Val Val Val Ser Arg Glu Leu His Thr Ser Ser Ala Arg Arg Trp 520
540

FIG. 2

(SEQ ID NO: 2)



TTTTTATGGG AATCGCAGCT TGGAAGAGAC AGARCAATTC CAGAAWTAAA TTGRAATTGA
AGATTTAACC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAACTTWAA
AAGGGRCTGC GCAGAGTAGC AGGGGCCCTG GAGGGCGCGG CCTGAATCCT GATTGCCCTT
CTGCTGAGAG GACACACGCA GCTGAAGATG AATTTGGGAA AAGTAGCCGC TTGCTACTTT
AACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAAATAATC CCATCAGAGT CTCACCCCCA
CATTCAATTA CTGAAAAGCA ATCGGGAAC TCTGGTCACT CACATCCGCA ATACTCAGTG
TCTGGTGGAC AACTTGCTGA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
TGCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGGTAC AGAGCAAGGG
CGAGGAGGTG TCCGAGTTCT TCCTCTACTT GCTCCAGCAA CTCGCAGATG CCTACGTGGA
CCTCAGGCCT TGGCTGCTGG AGATCGGCTT CTCCCCTTCC CTGCTCACTC AGAGCAAAGT
CGTGGTCAAC ACTGACCCAG TGAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCCG
TGA CTCCAAG TTCGTGCTGT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
CCTGGCCTGC CTCCTGGACC ACACCACCGG CATCCTCAAT GAGCAGGGTG AGACCATCTT
CATCCTGGGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
GGCCACGGGC CGGCTAGACG CAGGGGTCAA ATTCTTCTTC CACTTTCGCT GCCGCATGTT
CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGCCTTCCTG CTGCGCTTCC CCCACGTGGC
CCTCTTCACC TTCGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTGA GCCGCGTGCC
TGACAGCTCC TGCCCCCTGGG AGCCTGCCCCA CCCCCTGGTC TTGCTGGCCA ACCTGCTCAG
TGGGAAGCTG CTCAAGGGGG CTAGCAAGCT GCTCACAGCC CGCACAGGCA TCGAGGTCCC
GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTGCGCGC
CTATGCCAGG AGGATGTTCC CCGAGCGGGC CCTGCAGGAC CGCCTGCTGA GCCAGCTGGA
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GTGCTTCCAG CACTTCCGTG CTGCCTTTGA AGGCTCACCA CAGCTGCCCCG ACTGCACGAT
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CAGCCTGGTG CAGCGGAACA CACGCAGCCC AGTGGAGACC CTCCACGCCG GCCGGGACAC
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GGCTTTGCCG GAGCTGGGCC CCGGGGGTGA CCAGCAGTCC TATGAGTTTT TCCACCTCAC
CCTCCAGGCC TTCTTTACAG CCTTCTTCCT CGTGCTGGAC GACAGGGTGG GCACTCAGGA
GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCCTGCGGGG GCAGCGACCA CGTCCTGCTA

FIG. 3A



TCCTCCCTTC CTCCCGTTCC AGTGCCTGCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
CAAGAACAAG GATCACTTCC AGTTCACCAA CCTCTTCCTG TCGGGGCTGT TGTCCAAAGC
CAAACAGAAA CTCCTGCGGC ATCTGGTGCC CGCGGCAGCC CTGAGGAGAA AGCGCAAGGC
CCTGTGGGCA CACCTGTTTT CCAGCCTGCG GGGCTACCTG AAGAGCCTGC CCCGCGTTCA
GGTCGAAAGC TTCAACCAGG TGCAGGCCAT GCCCACGTTC ATCTGGATGC TCGCTGCAT
CTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGGCC AGGGGCATCT GCGCCAACTA
CCTCAAGCTG ACCTACTGCA ACGCCTGCTC GGCCGACTGC AGCGCCCTCT CCTTCGTCCT
GCATCACTTC CCCAAGCGGC TGGCCCTAGA CCTAGACAAC AACAACTCTCA ACGACTACGG
CGTGCGGGAG CTGCAGCCCT GCTTCAGCCG CCTCACTGTT CTCAGACTCA GCGTAAACCA
GATCACTGAC GGTGGGGTAA AGGTGCTAAG CGAAGAGCTG ACCAAATACA AAATTGTGAC
CTATTTGGGT TTATACAACA ACCAGATCAC CGATGTCGGA GCCAGGTACG TCACCAAAT
CCTGGATGAA TGCAAAGGCC TCACGCATCT TAAACTGGGA AAAAACAAAA TAACAAGTA
AGGAGGGAAG TATCTCGCCC TGGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTTGGGAT
GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TCGGGAACCA
CCCCAGCTTG ACCACCCTGA GTCTTGCGTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
CCTTGCGAGG GCCCTGCAGC AGAACACGTC TCTAGAAATA CTGTGGCTGA CCCAAAATGA
ACTCAACGAT GAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCAGC TGGCAGATGC
GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCCTAAAT GGAAACCTGA TAAAACCAGA
GGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTGT TTCTGAGAGG ATGCTTTTCT
GTTTATGGGG TTTTGGCCCT GGAGCCTCAG CAGCAAATGC CACTCTGGGC AGTCTTTTGT
GTCAGTGTCT TAAAGGGGCC TGCGCAGGCG GGAATATCAG GAGTCCACTG CCTYCATGAT
GCAAGCCAGC TTCCTGTGCA GAAGGTCTGG TCGGCAAACT CCCTAAGTAC CCGCTACAAT
TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
GAAAAAAAAA ACGGACGCGT GG (SEQ ID NO: 7)

FIG. 3B



MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCACPTQP
DKVRKIIDLVSQSGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVVNTDPVSRYT
QQLRHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSLACLDDHTTGILNEQG
ETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFRCRMFSCFKESDRICLQDILLFKHYCY
PERDPEEVFAFLLRFPHVAFVTFDGLDELHSDLDLSRVPDSSCPWEPAPHLVLLANLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCWIIIFRCFQHFRAAFEGSPQLPDCMTLTLDVFLVTEVHLNRMQPSLSVQRNTRSPVETLHA
GRDTLCSLQGVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELPGGDQQSYEFFHLLTL
QAFFTAFFLVLDLDRVGTQELLRFFQEWMPAGAAATTCYPPFLPFQCLQSGSPAREDLFKNKDH
QFTNLFLCGLLSKAKQKLLRHLVPAALRRKRKALWAHLFSSLRGYLKS LPRVQVESFNQVQAMP
TFIWMRLCIYETQSQKVGQLAARGICANYLKLTYCNACSDCSALS FVLHFFPKRLALDLDNNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGNKKITSEGGKYLA LAVKNSKSI SEVGMWGNQVGDGAKAFEAALRNHPSLTLTL
SLASNGISTEGGKSLARALQQNTSLEILWLTONELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQNTGITEICLNGNLIKPEEAKVYEDEKRIICF (SEQ ID NO: 8) **FIG. 4**



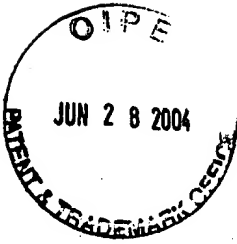
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AAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
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GATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
GAGCCTCTGGGCCACGGGCCGCTAGACGCAGGGGTCAAATTTCTTCTTCCACTTTCGCT
GCCGCATGTTTCAAGTTCAGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTT
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCACGTGGCCCTCTTACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCCTGACAGCTCCTGCCCTGGGAGCCTGCCACCCCTGGTCTTGCTG
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AGGCATCGAGGTCCCGCGCCAGTTCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
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AGCTGCCCCGACTGCACGATGACCCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCAT
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GGTGAATAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACCTGGGCCAGCAGAGCAT
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ACTACTAGATCACTTGTCTCTTGCCAGCTCATTTGTTAATAAAATACTGAAAACACAA
AA
AAAAAAAAAAAA (SEQ ID NO: 25)

FIG. 5



HASDLLKNDYFSAEDAEIVCACPTQDPDKVRKILDLVQSKGEEVSEFFLYLL
QQADAYVDLRPWLLLEIGFSPSLLTQSKVVVNTDPVSRYTQQLRHHILGRDS
KFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSLACLLDHTTGILN
EQGETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFRCRMFSCFK
ESDRCLQDILLFKHYCYPERDPPEEVFAFLRRFPHVALLTFDGLDELHSDLD
LSRVPDSSCPWEPAHPLVLLANLLSGKLLKGASKLLTARTGIEVPRQFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCMTLTLDVFLVTEVHLNRMQPSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFL
RALPELGPBGDQQSYEFFHLSLLTCKTGIPV (SEQ ID NO: 26)

FIG. 6



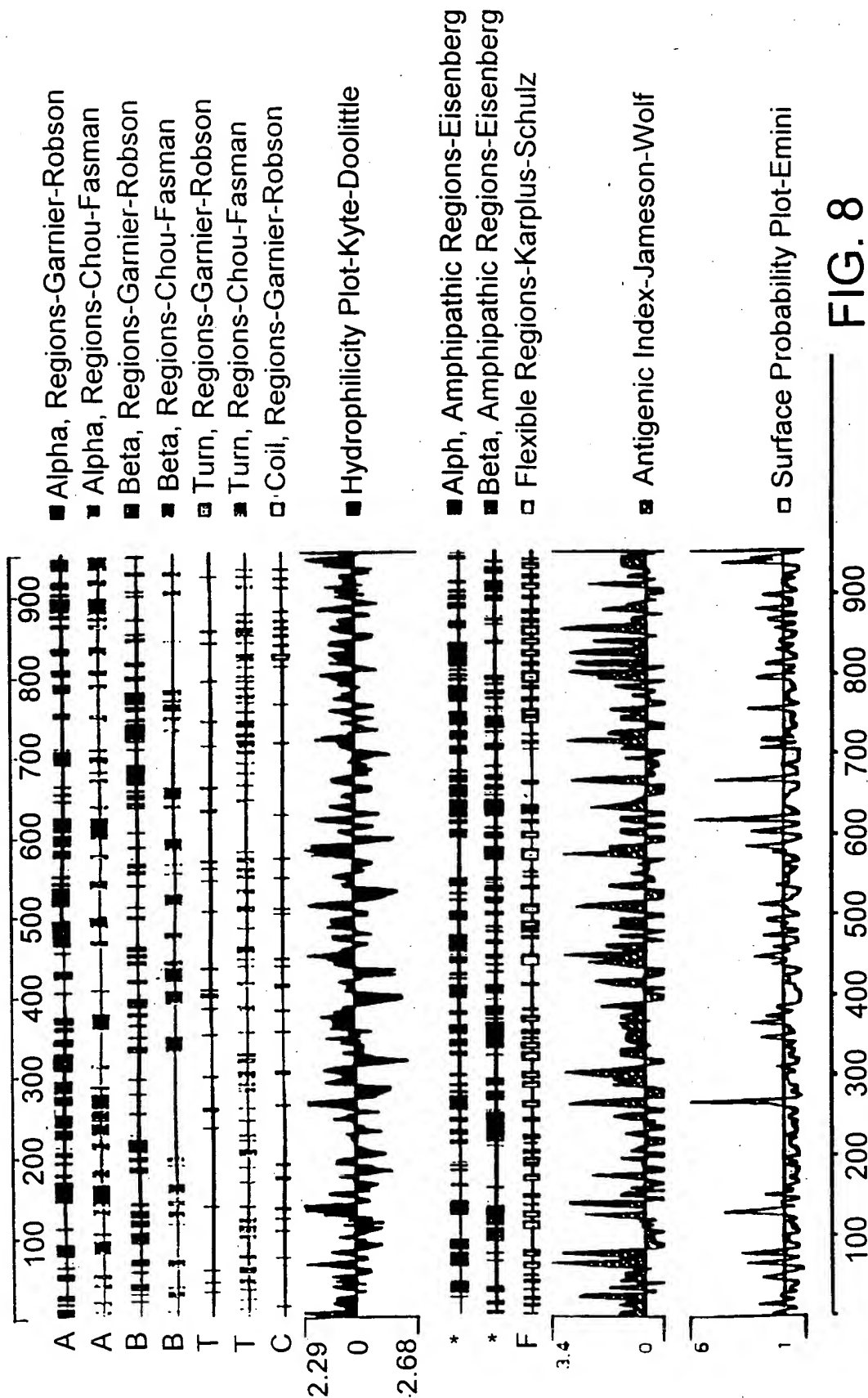
Applicant(s): John Bertin

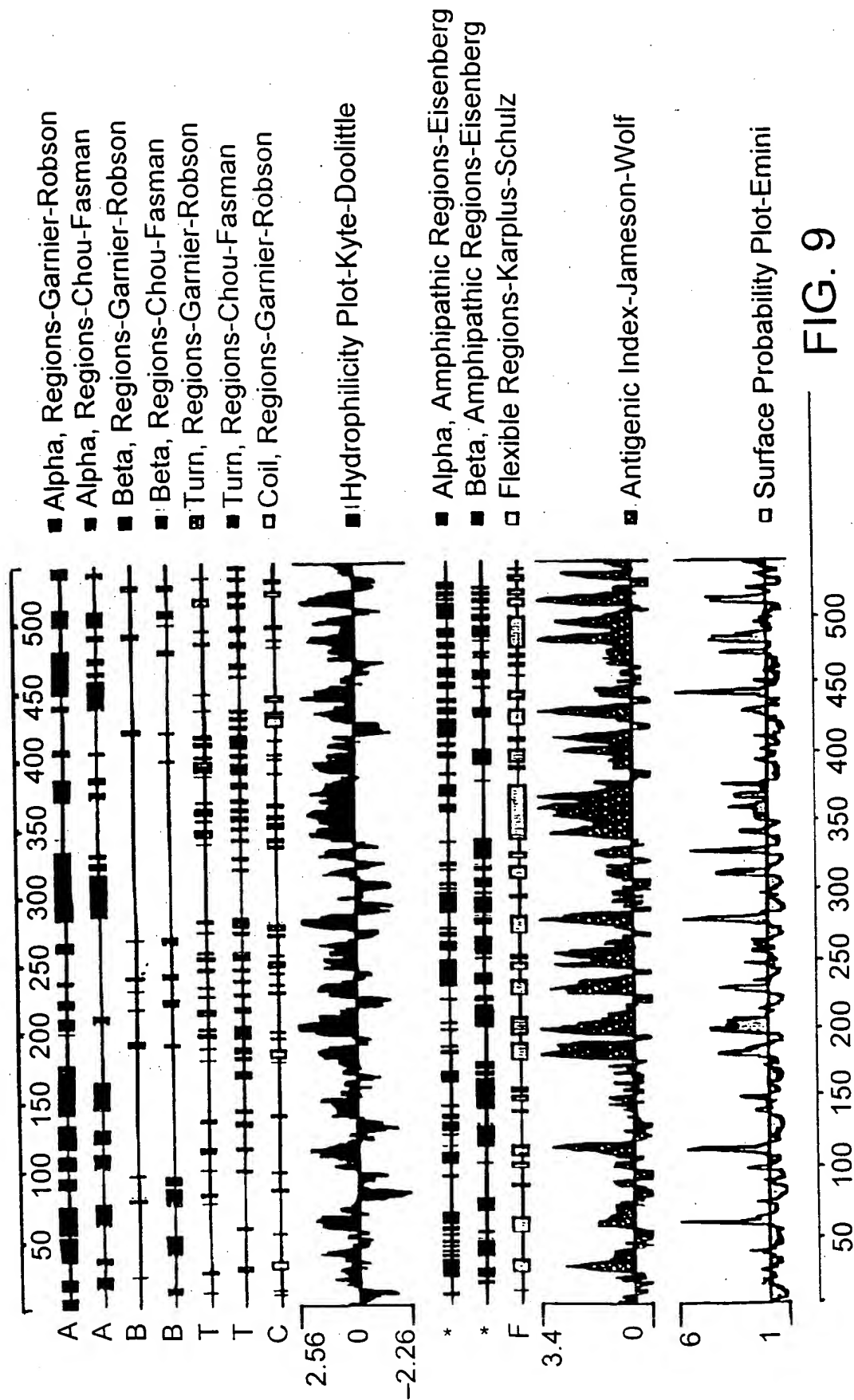
NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

SEQ. ID NO. 31/32/33/34

1	E	S	H	P	H	I	-	-	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	-	-	-	V	D	N	L	L	K	N	D	Y		CARD4-CARD		
11	L	-	Q	P	G	I	A	P	S	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD3-CARD			
11	A	Q	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD				
11	M	A	S	D	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD				
11	K	E	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD				
36	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	E	V	S	E	F	F	L	Y	L		CARD4-CARD		
39	I	M	K	E	D	Y	E	A	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	F	A	K	V	I	V	Q	K		CARD3-CARD	
37	L	T	G	P	E	Y	E	A	L	D	A	L	P	D	A	E	R	R	V	R	L	L	L	L	L	V	Q	G	K	G	E	A	A	C	Q	E	L	L	R	C		ARC-CARD		
36	I	N	K	Q	E	H	D	I	I	K	Q	K	T	Q	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	W	V	K	G	N	A	A	A	N	I	F	K	N	C		CIAP1-CARD
36	I	N	E	Q	E	H	D	I	I	K	Q	K	T	Q	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	L	V	K	G	N	I	A	A	T	V	E	R	N	S		CIAP2-CARD
76	L	Q	Q	L	A	D	A	-	-	Y	V	D	L	R	P	W	-	-	L	L	E	I	G	F	S	P	S	L	L															CARD4-CARD
79	L	K	D	N	K	Q	-	-	M	G	L	Q	P	P	Y	P	E	I	L	V	S	R	S	P	S	L	L																CARD3-CARD	
77	A	Q	R	T	A	G	A	-	-	P	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD		
76	L	K	E	I	D	S	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD		
76	L	Q	E	A	E	A	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD		

FIG. 7







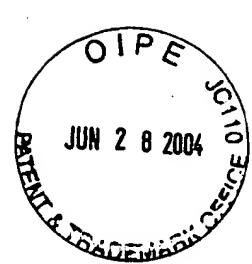
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CAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCCCTCTTCTGCTGGATCATCTTCCGGTG
CTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACACAGCTGCCCGACTGCACGATGAC
CCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCATCTGAACAGGATGCAGCCCAGCAG
CCTGGTGCAGCGGAACACACGCAGCCAGTGGAGACCCTCCACGCCGGCCGGGACACTCT
GTGCTCGCTGGGGCAGGTGGCCCACCGGGGCATGGAGAAGAGCCTCTTTGTCTTACCCA
GGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGAGACATGCAGCTGGGCTTCTGCGGGC
TTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCAGTCCTATGAGTTTTTCCACCTCACCT

FIG. 10A



CCAGGCCTTCTTTACAGCCTTCTTCCTCGTGCTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACGTCCTGCTATCC
TCCCTTCCCTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCGGCGCGGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCACCAACCTCTTCCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCCTGCGGCATCTGGTGCCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCCACGTTTCATCTGGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCCTTCGTCCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTGCGAGCCAGGTACGTCACCAAAATCCT
GGATGAATGCAAAGGCCTCACGCATCTTAAACTGGGAAAAAACAAAATAACAAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCACCC
CAGCTTGACCACCCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATGAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTTCCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCCTGCGCAGGCGGGACTATCAGGAGTCCACTGCCTCCATGATGCA
AGCCAGCTTCCTGTGCAGAAGGTCTGGTCCGCAAACCTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGCGAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCCAACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAAGTTGGTGCCAAGCTTCTTG
AATAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCCTTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTTGACTCCTCCAAGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

FIG. 10B



GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCTCCTCTAGAAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO: 38)

FIG. 10C

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVV
VNTDPVSRYTQQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSL
ACLLDHTTGILNEQAASRKVTGCVCRTCSSSTTATQSGTPRRCLPSCCASPTWPSSPSMA
WTSCRTWT (SEQ ID NO: 39)

FIG. 11



CACGCGTCCGCGCTACTGCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGCCCCG
GCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCTTTCGGTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAACATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCTGCCCCACCCAGCCTGACAAGGTCCGCAAATTTCTGGACCTGGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGCTGCTGGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGCCCAGGTGCTATTTTGATTTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATTCAAGGTTGTATTTTTTTTTCTTTAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAANGGGCGG (SEQ ID NO: 40)

FIG. 12

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPDKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVV
VNTDPGRSQPQQDRRHQCKQGPGGFGNGWASPECHLRKQAQVLF
(SEQ ID NO: 41)

FIG. 13



	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	Majority
											10										20																	30			40
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4-Y CLONE
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4-Z CLONE
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4L
	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	Majority
											50										60																	70			80
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4-Y CLONE
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4-Z CLONE
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4L
	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	Majority
											90										100																	110			120
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4-Y CLONE
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4-Z CLONE
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4L
	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	Majority
											130										140																	150			160
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4-Y CLONE
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4-Z CLONE
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4L

FIG. 14A



	- - - - -	T X X T X X X X P R - - - - -	- - - - -	- - - - -	- - - - -	Majority
	330		340	350	360	
212	- - - - -	T T A T Q S G T P R - - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
321	K L L K G A S K L L T A R T G I E V P R Q F L R K K V L L R G F S P S H L R A Y					CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	R C Majority
	370		380	390	400	
222	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
361	A R R M F P E R A L Q D R L L S Q L E A N P N L C S V P L F C W I I F R C					CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	Majority
	410		420	430	440	
224	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
401	F Q H F R A A F E G S P Q L P D C T M T L T D V F L L V T E V H L N R M Q P S S					CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	Majority
	450		460	470	480	
228	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
441	L V Q R N T R S P V E T L H A G R D T L C S L G Q V A H R G M E K S L F V F T Q					CARD4L

FIG. 14C



	- - - - - X X P X X X W - - - - -	Majority
	650 660 670 680	
235	- - - - - S S P S M A W - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
641	E S F N Q V Q A M P T F I W M L R C I Y E T Q S Q K V G Q L A A R G I C A N Y L	CARD4L
	- - - - - X X C X X X - - - - -	Majority
	690 700 710 720	
242	- - - - - T S C T R T - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
681	E L T Y C N A C S A D C S A L S F V L H H F P K R L A L D L D N N N L N D Y G V	CARD4L
	- - - - - - - - - - - - - - - - -	Majority
	730 740 750 760	
248	- - - - - - - - - - - - - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
721	R E L Q P C F S R L T V L R L S V N Q I T D G G V K V L S E E L T K Y K I V T Y	CARD4L
	- - - - - - - - - - - E C X - - - - -	Majority
	770 780 790 800	
248	- - - - - - - - - - - - - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - E C H - - - - -	CARD4-Z CLONE
761	L G L Y N N Q I T D V G A R Y V T K I L D E C K G L T H L S L Y N N Q I T D V G	CARD4L

FIG. 14E



	810	820	830	840	Majority
	---	---	---	W X X X X X X X X	
248	---	---	---	---	CARD4-Y CLONE
156	---	---	---	W T	CARD4-Z CLONE
801	A R L G K N K I T S E G G K Y L A L A V K N S K S I S E V G M W G N Q V G D E G				CARD4L
	---	---	---	---	
	X X X X X L R X X X X X X X X X X X X X X X X X X				Majority
	850	860	870	880	
249	---	---	---	---	CARD4-Y CLONE
156	---	---	---	---	CARD4-Z CLONE
841	A K A F A E A L R N H P S L T T L S L A S N G I S T E G G K S L A R A L Q Q N T				CARD4L
	---	---	---	---	
	X X X X L X				Majority
	890	900	910	920	
249	---	---	---	---	CARD4-Y CLONE
161	---	---	---	---	CARD4-Z CLONE
881	S L E I L W L T Q N E L N D E V A E S L A E M L K V N Q T L K H L W L I Q N Q I				CARD4L
	---	---	---	---	
	X X				Majority
	930	940	950	960	
249	---	---	---	---	CARD4-Y CLONE
164	---	---	---	---	CARD4-Z CLONE
921	T A K G T A Q L A D A L Q S N T G I T E I C L N G N L I K P E E A K V Y E D E K				CARD4L

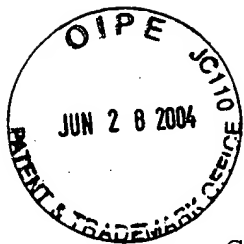
FIG. 14F



Majority	
	CARD4-Y CLONE
	CARD4-Z CLONE
	CARD4L
249	X X X X F
164	- - - F
961	R I I C F

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 14G



CCACGCGTCCGCGGACCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCCGCCCGAT
CCGCGACCCTAGTCCCCGGATCCCCTTGCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTTGTCACTCCACATTAAACTGCTGAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGGACAACTTGTCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCCTGTCCCACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGC
TCATTTCGGACCAAACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
GACACCAACTGGGCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCTCAACGAGC
ATGGCGAGACTGTCTTCGTGTTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGCATGTTTCACTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
GCTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCTGGGAGCCGGCTCACCTCTGGTCTGCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTCGCA
CAGGCGTGAGGTTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCCTATGCCCCGCCGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTCACCGCCTTCTTCCTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15A



CAAGCTCGTCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCGACAGAACTCCTTCGGCAGCTGGTGCCCAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCTTTCGTCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACTGACCA
AGTATAAGATCGTGACGTTCTTGGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAAATCCTGGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGGAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATTCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCGAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTCAGGAGC
CCACACCTCCACAGTGCACACCGATGTCCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCACCACTCAAAGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTC
ACCTTCAGAAAAGAGCTGGGAACTTGAGCAGAGCCGATGGTAACTTCTTGGGGAAAGAAG
GCACCCAGTGA CTGCATGGTTATTCTGAGTCCTCCTTCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTCGGTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTCAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCCAACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

FIG. 15B



CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTGAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGCCAG
TTCATTTGTTAATAAAATATTTAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO: 42)

FIG. 15C

MEEHGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLENGYFSAEDAEIVCA
CPTKPKDKVRKILDLVQSKGEEVSEFFLYVLQQLDAYVDLRLWLSEIGFSPSQLIRTKTI
VNTDPVSRYTQQLRHQLGRDSKFMLCYAQKEDLLEETYMDTLMGLVGFNNENLGS LGGL
DCLLDHSTGVLNEHGETVFVFGDAGVGKSMMLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLS LQDLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCPWEPAHPLVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFSPSHLRAY
ARRMFPERTAQEHL LQQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFHLLTQAFFTAFFLVADDKVSTREL
LRFFREWTS PG EATSSSCHSSFFSFQCLGGRSRLGPD PFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGR LAARGISADY LKLAFCNACSADCSALS FVLH H FHRQLALDLDNNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGKNRITSEGGKCV ALAVKNSTSIVDVGMWGNQIGDEGAKAF AEAL KDHP
SLTTLSLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF

(SEQ ID NO: 43)

FIG. 16



MEEOGHSEMEGIPLGSHSHIOLKINRELLVNTIRNTQCLVDNLLNGYFSAEDAIEVCACPTQPKVKRILDLVQSKGEEVSEFFLYVL
10 20 30 40 50 60 70 80 90
MEKHGHMEGTPLGCHSHIKLKLINREHLVNTIRNTQCLVDNLLNGYFSAEDAIEVCACPTQPKVKRILDLVQSKGEEVSEFFLYVL 90
NEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAIEVCACPTQPKVKRILDLVQSKGEEVSEFFLYLL 90

QQLADAYVDLRLLLEIGFSPSLLIOSKVWVNTDPVSRYTOOLRHOLGRDSKFVLCYAKEDLLLEEIYMDTLMGLVGFNLSGLGGL
100 110 120 130 140 150 160 170 180
QCLEDAYVDLRLLSEIGFSPSLLIRTKTIWNTDPVSRYTOOLRHOLGRDSKFVLCYAKEDLLLEEIYMDTLMGLVGFNLSGLGGL 180
QQLADAYVDLRLLLEIGFSPSLLIQSKVWVNTDPVSRYTOOLRHHLGRDSKFVLCYAKEBELLLEEIYMDTIMELVGFNLSGLSLSL 180

ACLLDHSTGVINEOGETVFLGDAGVGKSMLLQRLQSLWASGRLTAGAKFFHFHRCRMFSCFKESDRLSLODLLFKHFCYPEODPEEVFA
190 200 210 220 230 240 250 260 270
DCLLDHSTGVINEHGETVFLGDAGVGKSMLLQRLQSLWASGRLTSTAKFFHFHRCRMFSCFKESDMLSLODLLFKHFCYPEODPEEVFS 270
ACLLDHTTGILNEQGETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFHRCRMFSCFKESDRLCLODLLFKHYCYPERDPEEVFA 270

FLLRFPHVAFITFDGLDELHSDLDLSRVPDSCCPWEPAPHLVLLANLLSGKLLKAGAKLLTARTGVEVPROLLRKKVLLRGFSPSHLRAY
280 290 300 310 320 330 340 350 360
FLLRFPHTALFTFDGLDELHSDLDLSRVPDSCCPWEPAPHLVLLANLLSGRLLKAGAKLLTARTGVEVPROLLRKKVLLRGFSPSHLRAY 360
FLLRFPHVAFITFDGLDELHSDLDLSRVPDSCCPWEPAPHLVLLANLLSGKLLKAGAKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAY 360

ARRMFPERAAQDHLLSOLDANPNLCSLCGVPLFCWIIIFRCFQHFQAAFEQSSQLPDCAVTLTDVLLVTEVHLNRMOPSSLVQNRTRSP
370 380 390 400 410 420 430 440 450
ARRMFPERTAQEHLLQOLDANPNLCSLCGVPLFCWIIIFRCFQHFQVFEQSSQLPDCAVTLTDVLLVTEVHLNRMOPSSLVQNRTRSP 450
ARRMFPERALQDRLLSQLEANPNLCSLCVPLFCWIIIFRCFQHFRAAFEGSP-QLPDCTMTLTDVLLVTEVHLNRMOPSSLVQNRTRSP 449

AETLHAGRDTHALGEVAHRTKSLFVFGQEEVOASGLOEGDLOLGLRALPDVPGCGDQSGSYEFFHLLTLOAFFTFFLVADDKVGTOE
460 470 480 490 500 510 520 530 540
AETLRAGWRTLHALGEVAHRTKSLFVFGQEEVOASGLOEGDLOLGLRALPDVGPPE-QQSYEFFHLLTLOAFFTFFLVADDKVGSTRE 539
VETLHAGRDTHALGEVAHRTKSLFVTEEVQASGLQERDMQGLRALPELPGDQDQSYEFFHLLTLOAFFTFFLVADDKVGTOE 539

FIG. 17A



LLRFFQEWISPGGAASSCHSSFLSFOCLGSGRAGEDLFKNKDHFQFTNLFVCGILLAKAKOKLLROLVPAAALRRKRKALWAHLFASLR 550 560 570 580 590 600 610 620 630 629
LLRFFREWTSPGEATSSSCHSSFFSFOCLGSRSLGPDPPFRNKDHFQFTNLFVCGILLAKARQKLLRQLVPKAILRRKRKALWAHLFASLR 629
LLRFFQEWMPAGAAITSCYPPFLPFQCLQSGSPAREDLFKNKDHFQFTNLFVCGILLSSKAKQKLLRHLVPAAALRRKRKALWAHLFSSLR 629

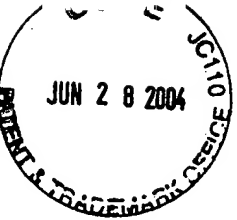
GYLKS LPRVQGGFNQVQAMPTFLWMLRCIYETOSQKVGOLAARGISADYLLKAFNCACSADCSALSFVLHFFHKOLALDLDNNNNLNDYG 640 650 660 670 680 690 700 710 720 719
SYLKS LPRVQSGGFNQVHAMPTFLWMLRCIYETOSQKVGRLAARGISADYLLKAFNCACSADCSALSFVLHFFHRQLALDLDNNNNLNDYG 719
GYLKS LPRVQVESFNQVQAMPTFIWMLRCIYETOSQKVGOLAARGICANYLKLTYCNACSDCSALSFVLHFFPKRLALDLDNNNNLNDYG 719

VOELQPCFSRLTVLRSLVNOITDGGVKVLSEELTKYKIVTFLGLYNNQITDVGARYVAQILDECKGLTHLSLYNNQITDVGAKLGKKNKIT 730 740 750 760 770 780 790 800 810 797
VOELQPCFSRLTVLRSLVNOITDGGVKVLCEELTKYKIVTFLGLYNNQITDVGARYVAQILDECRGLKHL-----KLGNRIT 797
VRELQPCFSRLTVLRSLVNOITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKILDECKGLTHLSLYNNQITDVGARLGKKNKIT 809

SEGGKYVALAVKNSTSIIVDGMGNQVDEGAKAFAEALKDHPSLTTLSLASNGISTEGGKSLAQALQONTSLTVLWLTQNELNDEVAES 820 830 840 850 860 870 880 890 900 887
SEGGKCVLAVKNSTSIIVDGMGNQVDEGAKAFAEALKDHPSLTTLSLAFNGISPEGKSLAQALKONTTTLTVLWLTQNELNDESAEC 887
SEGGKYLAVKNKSKI SEVGMGNQVDEGAKAFAEALRNHPSLTTLSLASNGISTEGGKSLARALQONTSLLEILWLTQNELNDEVAES 899

LAEMLKVNQTLKHLWLIQNIITAKGTAQALADALQNSNTGITEICLNGNLKPEEAKVFEDEKRIICE 910 920 930 940 950 960 953
FAEMLRVNQTLRHLWLIQNIITAKGTAQALARALQNTAITEICLNGNLKPEEAKVFENEKRIICE 953
LAEMLKVNQTLKHLWLIQNIITAKGTAQALADALQNSNTGITEICLNGNLKPEEAKVFEDEKRIICE 965

FIG. 17B



tgtatgattctgtttatatgaaatgtccagaaaaggtaaattctatagacaaagcaaattcagtagt
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FIG. 18B



ctgtcacaccagtggtcagagtgtaataaattgcatggggacatgggggtgcaggggggtcgaaggct
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FIG. 18C



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FIG. 18D



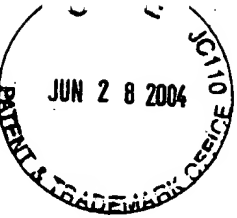
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FIG. 18E



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FIG. 18F



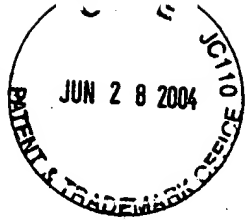
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FIG. 18G



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FIG. 18H



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aacctgctcagcaggatgagagtggtccattcactaagccaggggaccctaggagggtgtggctac
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ctcagatgtagaggtcacatggaggagaatataggaaaggaaattgaagtagagtgctcagatgc
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gaggtcaggacagccaaaatcctgaggggccaagaaagacaagacctggaaaatgtcattaaattc
aggcttatggaggctacaggtgaccttagtgagaccagtgaaacagaggggatggcagctggagag
gatccatgctaataatgaaggaaactatctgcaaagggtatgttcccttaatttcagggatacatgtg

FIG. 181



tattgtgtgatacacgagtggtgtgctatgaacacaccttgggaaggagtggtgcgaggatccttaa
cattttacctgtgtacttttgtcttcctccttttcaacagcctaaatggaaacctgataaaacca
gaggaggccaaagtctatgaagatgagaagcggattatctgtttctgagaggatgctttcctgtt
catgggggttttggcctggagcctcagcagcaaatagccactctgggcagtcttttgtgtcagtggt
cttaaaggggctgctgcgcaggcgggactatcaggagtgccactgcctccatgatgcaagccagcttc
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FIG. 18J

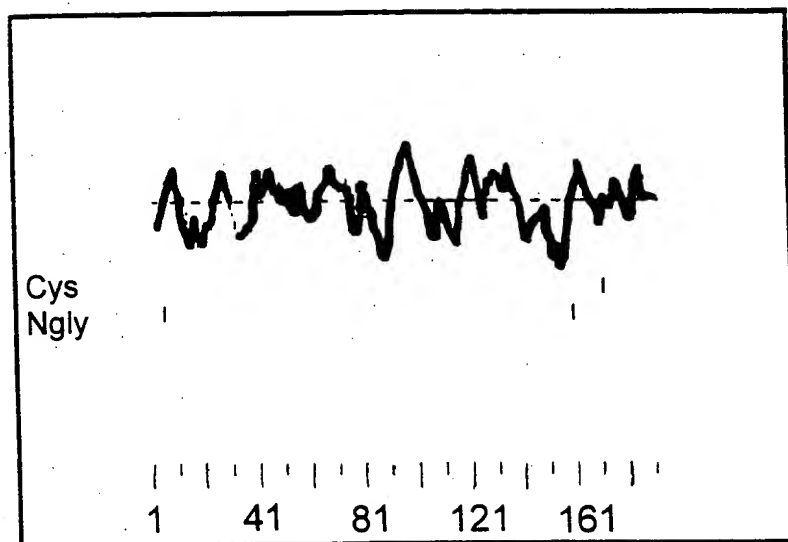


FIG. 20

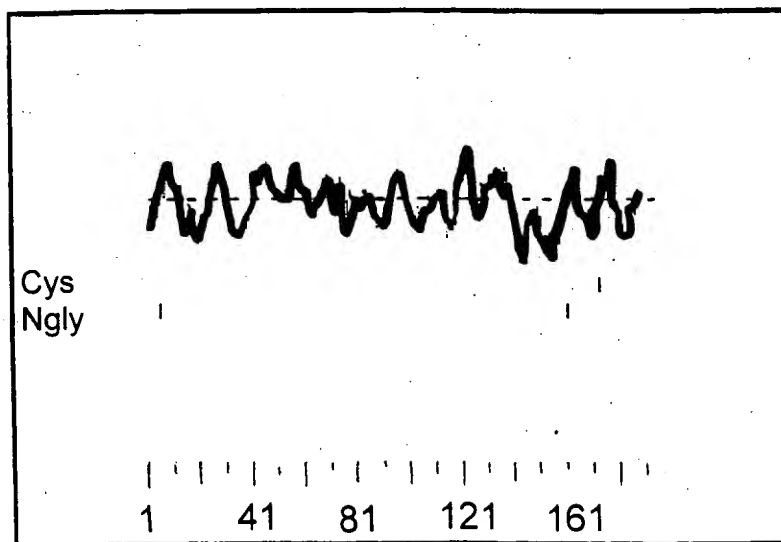


FIG. 22



1 CGCGTCCGGCTGCAGCGGGGTGAGCGGCGGCAGCGGCCGGGGATCCTGGAGCCATGGGGC
GCGCAGGCCGACGTGCGCCCACTCGCCGCGCTCGCCGCCCCCTAGGACCTCGGTACCCCC

1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTCGGTGCCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTTCGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCCGCTAGGGCGCCCCGC
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCGCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTGACCAAGTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCG
GGATGCCCGCGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGACGTCTCTACCGGC
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
CCGTCGACGTCCGCGGTGCGTGGTCCCGAGACCTCGGCGCGGTGACCCCTAGGTCCGGG
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTCCGTTCCGTCGCGACGTGAAATATCTGGTCGTGGCCCGACGCGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG
AGCGCTCCCAAGTGTGCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCAGGCGGAGCCCAACCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTCACGCCCCGGCTCGGGTGGTTGGGTTCTTACGCCCTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTCACACCAGCCTGGAAGTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCGGACCTTGACCTGGACGTTCTGAACGAGGAGGTCCGGGATTCCC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCAGCAACAC
TCAGGGTCAGGATGGACCACTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCTGGCAATCCCAACCAATCATCCTGAATCTGATCTTTTTATACACAAT
AGGCCAGTCGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACCTT

FIG. 21



ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-DNA 740 aa vs.
> mCARD5-DNA 763 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

68.2% identity; Global alignment score: 2377

```

      10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  ::::::::::: :::: :  :::: :::::  :::
      CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGGTGAC
      10      20      30      40      50      60

      40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGACGCCATCCTGGATGCGCTGGA
      :: :: :  :: ::::::::::: :::: :  ::::::::::: :::: :
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
      70      80      90      100     110     120

      100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTGCGGTGCCGCTGCG
      :::: :::: :  :: ::::::::::: ::::::::::: ::::::::::: :::::
      AAACTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
      130     140     150     160     170     180

      160     170     180     190     200     210
inputs CGAGGGCTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      ::::::::::: ::::::::::: :::: :  :::::  ::::::::::: :::::
      AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
      190     200     210     220     230     240

      220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCCTAAC-GTGC
      ::::: :  ::::::::::: ::::::::::: :::: :  ::::::::::: . :::: :
      TGACAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
      250     260     270     280     290

      280     290     300     310     320     330
inputs TCGCGGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  ::::::::::: ::::: :  ::::::::::: :  :::: :
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

      340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
      ::::: :  ::::: .  :  :  ::::: :::::  ::::::::::: :::: :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCTTGCTCAGAGTACAGCCAGAACAGG---AC
      360     370     380     390     400     410

      400     410     420     430     440     450
```

FIG. 23A



ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hCARD5-protein 195 aa vs.
> mCARD5-protein 193 aa
scoring matrix: paml20.mat, gap penalties: -12/-4
71.8% identity; Global alignment score: 712

```

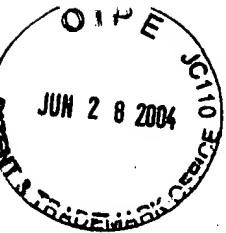
      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTKLVSYY
      10      20      30      40      50      60

      70      80      90     100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90     100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDAHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTCKDSSLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      ...
      LKEIHPYLVMDLEQS
      180     190
```

FIG. 24



1 CCCGCGTCCGGAAGTTCCTTCCAGTGTGTTGTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTTG
GGGCGCAGGCCTGAAGGGAAGGTCACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAC

66 GCATGTTTTATCTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACACG

131 CAGAATGACCTGATCCATTTCTGGTTTTGTAGAAAGCCATGGCTTCAGAGGGTGCTTCCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAACATCTTTCCGTACCGAAGTCTCCCACGAAGGAGTCTT

1 M A S E G A S S E

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTCCAACAAGATCCCGACTCTATCTTGGA
TAGTATCTTTTTGTGCGTTGTTTCAACGAGTCACAGGAGGTGTCTTAGGGCTGAGATAGAACCT

10 I I E K Q R T K L L S V L Q Q D P D S I L D

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCCTCCTCATACTCTGAGATCTCCGTTAATGTCTAG

31 T L T S R R L I S E E E Y E T L E A I T D

326 CTCTGAAGAAAAGCCGGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTTGT
GAGACTTCTTTTCGGCCTTCGACAATTAATACTAGGTCTTCTCCCTCTCCTGTGACAACAACA

53 P L K K S R K L L I L I Q K K G E D S C C C

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTACAGACAGATTACGGAAGGTGTGAGTCGAAGGTGGAACCCAAATTTCTGCTCTCA

75 F L K C L S N A F P Q S A S T L G L K Q E V

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGAAGATCCCTTTTCTCTTG
AGGTGCCGTCCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAACCTTCTAGGGAAAAGAGAAC

96 P R Q G T G E V V E V S R G L E D P F S L

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGGTCTGGGAGCTCCG
CCTGGTATTGGGGTCTTTATCGTCTCGAGAGTCTTCTCTTTCTTACGGGCCCAGACCCTCGAGGC

118 G T I T P E I A E L S E E K E C P G L G A P

586 GAGTTCTTACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAGTGGACGTTCTTTTCGTGCGGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT

140 E F F T C K E S S H R E P E V P S W E N Q E

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTTCAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCACGTGTGTTTCAAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTTCAAGGTC

161 G R G A Q Q V T A P R S V K G V E Y E V P

FIG. 25A



716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTCCGCTGTACTTAGAA
GTTTCATAGAGGGAGAATTTCGCTGCCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT

183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCTGAAGATGTTTTGGAGGAAGGGGCCGCGATGA
CTTCCCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCCGGCCGCTACT

205▶ E G E G E E S L G Y P E D V L E E G A G D D

846 CCCACAGTGCTTTGTATATGATAGTGAGGAGGAATGCCAGTATGAGGAAAACATGGGCTCCTCCG
GGGTGTCACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC

226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
CACTTCTGTGTCATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCCTCTTTTCGCGA

248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTTTTCAACACGTCCTGTCTCTTTGAACATGGATAGAAACAGAAAGCT
CTTCTTTCTTTTCTCACAAGTTGTGCAGGACAGGACAAACTTGTACCTATCTTTGTCTTTTCCA

270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCCAGAGTTTCGTGAGGCAGTTTTCCATAGACCGAGGATGTGAGTGGACACCCAAGACCCCAG
AGAGGGTCTCAAGCACTCCGTCAAAGGTATCTGGCTCCTACACTCACTGTGGGTTCTGGGGTC

291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGAATTTCTTGATGAAAGTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG

313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGGCCGACCTTATCTCTTCAATCCGTA

335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCCTGGATGTCCTCTGCGCCTGCATGCTTTGTGTCAGACAGCT
ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGGACGTACGAAACACGTCTGTCTGA

356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGCAGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTTGCTCTTCCCCTGCTACTGCCA
GGAACGTTCGCACTTCAGTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACGGT

378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P

1366 GATGCTGAGAACAACAAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
CTACGACTCTTGTGTGTTTTGGAGAATTACCATCCCCGGTACTTCTGGAATTTTCGTCGGGAGTCCG

400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25B



1431 ACAGTCCTCAGGAGGGCCCCCTCAGGGAAACAGACACATTTCTGGGTCTCACAAAGATGCCTGTCA
TGTCAGGAGTCTCCCCGGGAGTCCCTTTGTCTGTGTAAAGACCCAGAGTGTCTACGGACAGT
421▶ Q S S G G P L R E T D T F L G L T K M P V

1496 TCTCTTTTGTGCGACTAGGACGCTGCAGCTTCTCCAAGTCCAGAATTGTTAACACACTGCTCAGC
AGAGAAAACACGCTGATCCTGCGACGTGGAAGAGGTTTCAAGTCTTAACAATTGTGTGACGAGTCTG
443▶ I S F V R L G R C S F S K S R I V N T L L S

1561 TCCTCCCAGCAGAAACCATACCCGATTTTCTCCATCAGGATCTGTCTGTCCCTGTGCTTCTCTG
AGGAGGGTCTCTTTTGGTATGGGCTAAAAGGAGGTAGTCTTAGACAGACAGGGACACGAAGGAGC
465▶ S S Q Q K P Y P I F L H Q D L S V P V L P R

1626 GCAAATTTCTGACGGCCTGGTGAAGTGACATGGTGCTTTCTGACAAGTTGCTGAAGGAAAGCC
CGTTTAAAGACTGCCCGACACCTTCACTGTACCACGAAAGGACTGTTCAACGACTTCTTTTCGG
486▶ Q I S D G L V E V T W C F P D K L L K E S

1691 CGCATGCTTTCCAGAAACCTGTGTGCTGTGGCCAACCTTCGTGGAGATTTAGAAAGCTTTTGGATA
GCGTACGAAAGGTCTTTGGACAACGACACCGGTTGGAAGCACCTCTAAATCTTTGAAAACCTAT
508▶ P H A F Q K P V A V A N L R G D L E S F W I

1756 CAATTTGGTTTCTCTGGTAGAAGTTTCTCCGGTCTTTTCTTTTTCACAGACTGCCTTGGTGAGAA
GTTAAACCAAAGGACCATCTTCAAAGGAGGCCAGAAAAGAAAAAGTGTCTGACGGAACCACTCTT
530▶ Q F G F L V E V S S G L F F F T D C L G E K

1821 GGAATGGGACTTGCTAATGTTTTTAGGAGAGGACACCATTGAACGGTGCTACTTTATCCTCAGTC
CCTTACCCTGAACGATTACAAAAATCCTCTCTGTGGTAACTTGCCACGATGAAATAGGAGTCAG
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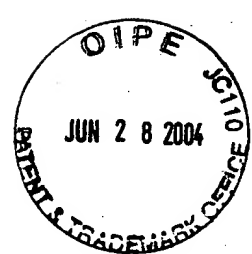
1886 CCCAGGCTAAGGAGAGTGAAGAAGCCCAGATTTTCCAAAGGATCCTAAAACTGAAGCEATCTCAG
GGGTCCGATTCTCTCACTTCTTCGGGTCTAAAAGGTTTCTTAGGATTTTGACTTCCGTAGAGTC
573▶ P Q A K E S E E A Q I F Q R I L K L K P S Q

1951 CTACTGTTTTTGGGAAGCTGAGGAAGCTGGGGATAGAAGGAAGACTATGGAGGCCCTTCAAGCTGC
GATGACAAAACCTTCGACTCCTTCGACCCTATCTTCTCTGATACCTCCGGGAAGTTCGACG
595▶ L L F W E A E E A G D R R K T M E A L Q A A

2016 CCTCCAGGAAGTAATGTCCTCTCCACTCAGATGTGTGTCCCTTGAAGAGATGGCCTCTCTGGCCA
GGAGGTCCTTCATTACAGGAGAGGTGAGTCTACACACAGGGAAGTCTCTACCGGAGAGACCGGT
616▶ L Q E V M S S P L R C V S L E E M A S L A

2081 GGGAGCTGGGCATTTCAGGTAGACCAAGACTTTGAAGTTACTCAAGATATTCAAGTTTCCCCACA
CCCTCGACCCGTAAGTCCATCTGGTTCTGAAACTTCAATGAGTTCTATAAGTTCAAAGGGGTGT
638▶ R E L G I Q V D Q D F E V T Q D I Q V S P T

FIG. 25C



2146 ACAGTTGAAGGTGAAAACCAACAACCATGTAGTCAGACCAAAAGCCCGGCTGAAAGCGGAGCTCA
TGTCAACTTCCACTTTTGGTTGTTGGTACATCAGTCTGGTTTTCGGGCCGACTTTCGCCTCGAGT
660▶ T V E G E N Q Q P C S Q T K S P A E S G A Q

2211 GGAGCCAATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTCCATCAGA
CCTCGGTAGTCTCTCGGTCCCCGAGTTACACTGCTGTCTAGTCTTACGAGGCCAAAAGGTAGTCT
681▶ E P I R E P G A Q C D D S Q N A P V F H Q

2276 CTCCAGTATACATGCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAGCTGGAGGTAACCTT
GAGGTACATATGTACGGAATAGGTCTGTGGGTACCCGAAACCGGTAGTTTCGACCTCCATTGAAA
703▶ T P V Y M P Y P A H P W A L A I K A G G N F

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCACAGCAGAGGGCTAAG
ATGGTGAAGGAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTCTCTCCCGATTC
725▶ Y H V P L N A P W L W A P T L D H S R G L S

2406 TGGTTCTTTCCATTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
ACCAAGAAAGGTAAGGGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGACGGTGGTAG
746▶ G S F H S H A K P T H S K A F Q A N C H H

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGCTAACCCCACTCATGTGCAG
GGTAGGGAGGGTACGATTTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAAGTACACGTC
768▶ P H P S H A K P T H V N P S H A N P T H V Q

2536 CCTTGCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
GGAACGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGAGGTGAGGGAGAGTCTGGAGA
790▶ P C M L N P L T L R P S K L N P L P L R P L

2601 TGGAGCCAAGCTAACTGCAATCATGCCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
ACCTCGGTTGATTGACGTTAGTACGGGTAGGGAGGGAACGATTTGGGAGAGTATGCTTAGGGAG
811▶ G A K L T A I M P I P P L L N P L I R I P

2666 TGATGCTAACCCCACTCATGTGCAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAAA
ACTACGATTGGGGTGAAGTACACGTCGGAAGGGTACGATTTGGGCGAGTAGATGTCAGAAGGGTTT
833▶ L M L T P L M C S L P M L N P L I Y S L P K

2731 CAAAACCTCCCCATCCCAATCTACTGCAGTTTACGGCACACAAACCTCAGCAGTCCCAGTCTAA
GTTTTGGGAGGGGTAGGGTTAGATGACGTCAAGTGCCGTGTGTTGGAGTCGTCAGGGTCAGATT
855▶ Q N P P H P N L L Q F T A H K P Q Q S Q S K

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCCAGACCAAGCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCTCTGGGTCAAGTCGATTTAGTAAGGTCTGGTTCGGAAGTGTCCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

FIG. 25D



2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGATGAGACCTCTAGACCCCTTATTTTCATACCCGA

898 C H P R A G R R

2926 TTGCTTAAGTATTCTTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAGT
AACGAATTCATAAGAAAAGTATATCGTTTCGACTTCTTTTCAAAATCATTCTGACTATTTTCA

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTCATACGTTTCAGAAATTCACGTATCGTTTCATAGGTTACACCCCTTAT

3056 TGGAAGCAGTTAAAAGTAGAATCTGGCTGGGCATGGTGGCACACATCTACAGGGTTTACGATGGG
ACCTTCGTCAATTTTCATCTTAGACCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC

3121 AGGGCTCTGTCATCCCAACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAACTCCGGTCAGACCAGA

3186 ACATAACAACGACACAAGCAAGTCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG

3251 AAAAGGGTTGGATCTAACATCAAACCAAAGAAATCAGTCAAGTATTCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTTGGTTTCTTTAGTCAGTTCATAAGGTCTTCCGTAGTAATTA

3316 ACACTCAGTGGGTTACCACAACCAAACCATCTCGACAACCTAACCCCTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGTTGGTTTGGTATGAGCTGTTGATTGGGGGATTTCTCGTTCTTCCT

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCAATTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATT

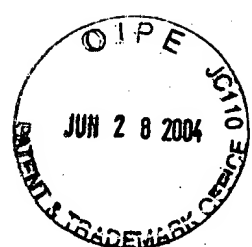
3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCTGAACAGTTTAGGTAATTTACGTTATAATTCTTCGTCACCCTTAGAATTCCGA

3511 ACATTAAGCTCCAGTGAGTCGCAACCCCTCCCCTATTAGATGATGTGAGATTTGAACCCCAAGTGAA
TGTAATTGAGGTCACCTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCATT

3576 TGGGGTGTGCTGATAGCCCGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAAATTTCACTACTTTTGCACCC

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCGATAGACACAACCTCTTTCCGACGAAGTCTCCACGGAACCAAAACCAATACTAGT

FIG. 25E



3706 GCCACTGAGCAGATACTCTGCACCATTTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCCAACGAAGACCATTTATCGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCTTTATTACTTACTAGTTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTCCTTTATATAATAGCTAAGAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTTCTGATATATTAGTTTTAATGGTTTGAAGTCAGAAATGTGTTAGTTTTTAAATTTTAGAGT
TCCCAAGACTATATAATCAAATTACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAATATTGAGATGAATTTACAAAGCCTATAAGTAATGTTGAGAGGGTTATAATTTTT
ATTAACTTTTATACTCTACTTAAATGTTTCCGATATTCATTACAACTCTCCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAATATCTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAGTGTACCAAGAGTCAATAAAG
TAAACTAAGTCCATAAATTGGTCTCGACGAGAAATCAAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCTTGTGTTGACACTGGAATGTGAATTCCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTCGTGTATCACTCTGGTCCAGAGTTCTGTGTTTTTGATAGGTGGAAT

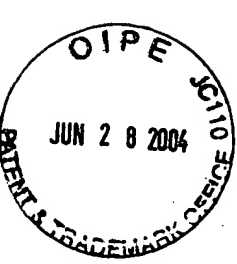
4291 AGGAAGATTTTTAAATTTGCCTCATTAAAGAAATAAAGTAAGATTTATAAATTGGACTAAATGTCA
TCCTTCTAAATTTTTAAACGGAGTAATTCCTTTATTTCATTCTAAATATTTAACCTGATTTACAGT

4356 CATCTTTGAACTTATGACTGTTTAATTTTTTGACTTAAAGTTTAATTTTATTATGTATGCGTGT
GTAGAACTTGAATACTGACAAATTAATAAAGTGAATTTCAAATTAATAAATACATACGCACA

4421 GTTGATGTGTGTGCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACACGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTCACACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAAATCGGGATACACAAAATGGGTGACTCGATCCGGTGGATGAGGATATTTCAG

FIG. 25F



4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTITACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTTAGCATAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTATACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTGCTGA
TACTAATAACATTTCTACTTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCTGTCTTTTAGAATGATAAATGTAAAGTAAAATAAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAATCTTACTATTTACATTCCTTCATTTTATTTTGCCAAGTAAGAGTCTTGTGA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCGGTCGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTCGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAATTTTATTCATCCTATATTTGTACATTTAATTGGGTGTGTAATACACCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTC
ACTCTTCGTCTTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCCTTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTTGTCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTAAAAAAGGGCGG
AATATTTTATTTGAGTGAAAATGAAAATTTTTTTTTTTTTTTTCCCGCC

FIG. 25G



NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

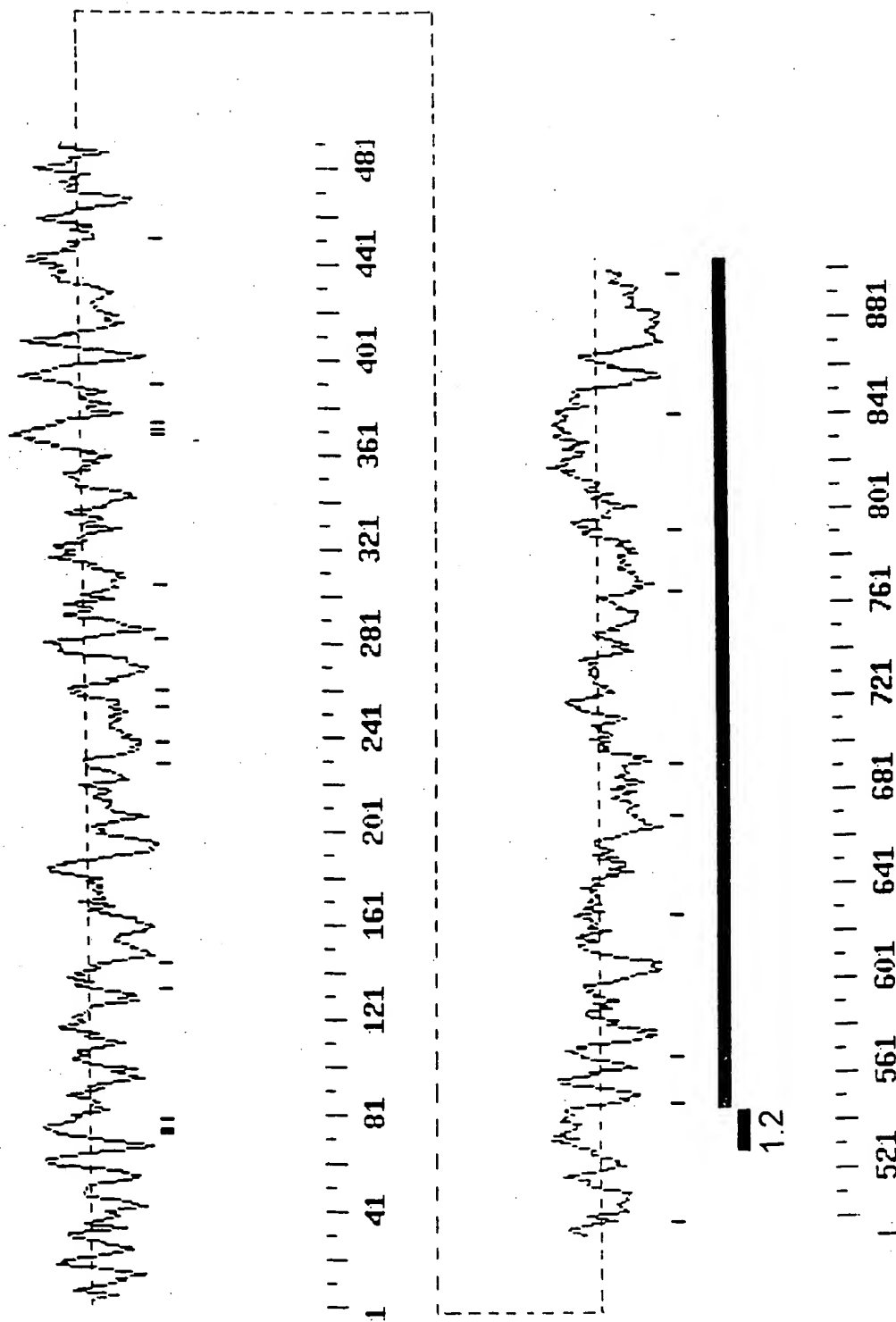
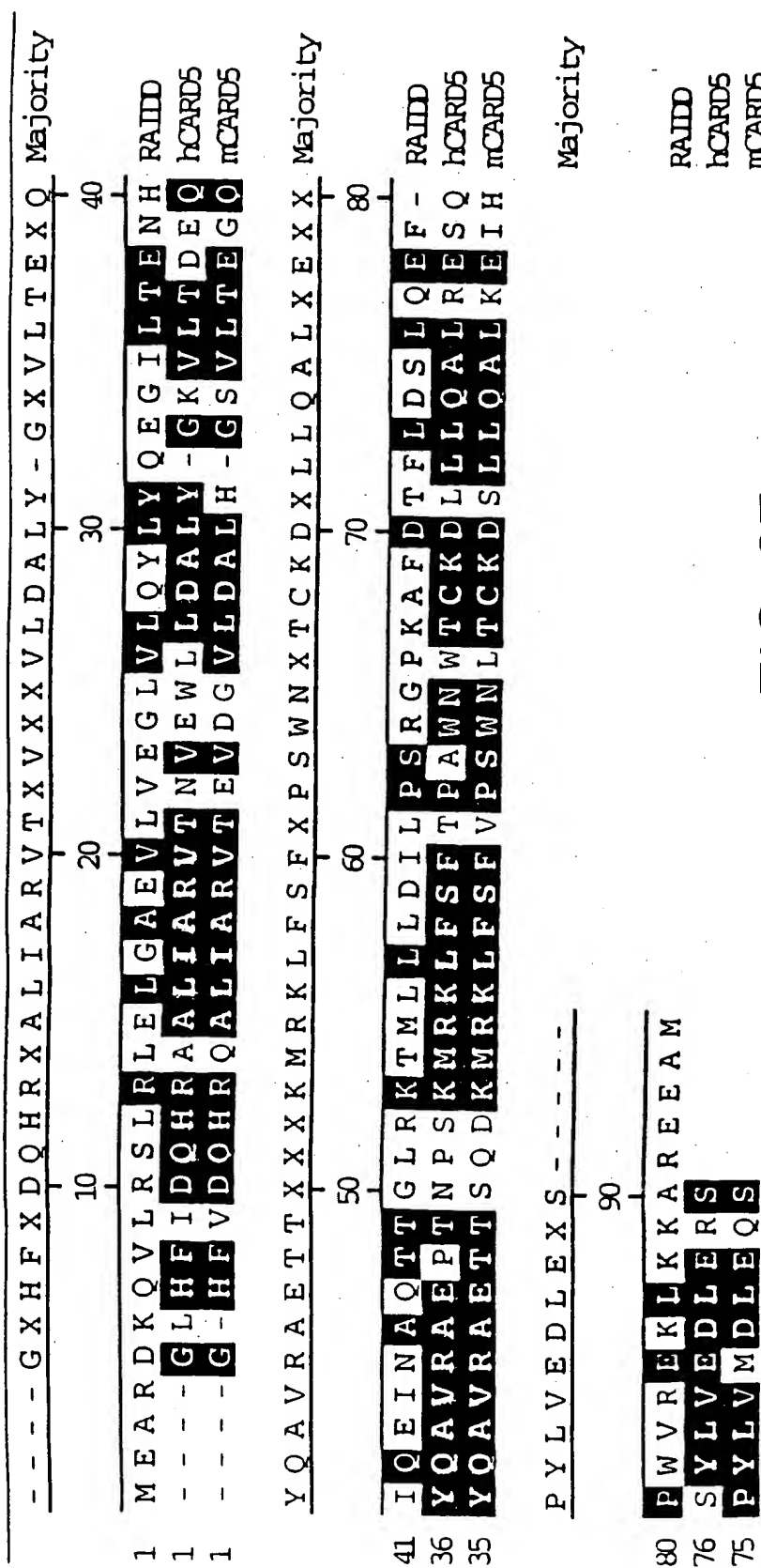


FIG. 26





CACGCGTCCGCCGATCAGAGAGTGCTCCGAGCTGGGTTGCCCCACTGTGCTTGTATCTGCACTCTCCAACACTAGGC 79

ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTGTGTCATTCTTTTTTAACTTTTACTTATTCATTAGGAT 158

M A T E S T P S E 9

GATTTCATAATATATTTCTCGGTTTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226

I I E R E R K K L L E I L Q H D P D S I 29

ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286

L D T L T S R R L I S E E E Y E T L E N 49

TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346

V T D L L K K S R K L L I L V Q K K G E 69

GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406

A T C Q H F L K C L F S T F P Q L A A I 89

GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466

C G L R H E V L K H E N T V P P Q S M G 109

TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526

A S S N S E D A F S P G I K Q P E A P E 129

GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586

I T V F F S E K E H L D L E T S E F F R 149

ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646

D K K T S Y R E T A L S A R K N E K E Y 169

GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706

D T P E V T L S Y S V E K V G C E V P A 189

GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766

T I T Y I K D G Q R Y E E L D D S L Y L 209

ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826

G K E E Y L G S V D T P E D A E A T V E 229

GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886

E E V Y D D P E H V G Y D G E E D F E N 249

GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946

S E T T E F S G E E P S Y E G S E T S L 269

TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006

S L E E E Q E K S I E E R K K V F K D V 289

TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066

L L C L N M D R S R K V L P D F V K Q F 309

CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126

S L D R G C K W T P E S P G D L A W N F 329

TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186

L M K V Q A R D V T A R D S I L S H K V 349

CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246

L D E D S K E D L L A G V E N L E I R D 369

CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

FIG. 28A



I Q T I N P L D V L C A T M L C S D S S 389
ATA CAA ACC ATT AAT CCC CTT GAC GTG CTT TGT GCC ACC ATG CTG TGT TCA GAT AGC TCT 1366

L Q R Q V M S N M Y Q C Q F A L P L L L 409
TTG CAA CGC CAA GTC ATG TCA AAC ATG TAT CAG TGC CAG TTT GCT CTT CCC CTG CTA CTG 1426

P D A E N N K S I L M L G A M K D I V K 429
CCA GAT GCA GAA AAC AAC AAA AGC ATC TTA ATG CTG GGG GCC ATG AAA GAC ATT GTG AAG 1486

K Q S T Q F S G G P T E D T E K F L T L 449
AAG CAG TCA ACA CAG TTT TCA GGG GGG CCT ACA GAG GAT ACA GAA AAG TTT CTG ACT CTC 1546

M K M P V I S F V R L G Y C S F S K S R 469
ATG AAG ATG CCT GTC ATC TCT TTT GTG CGT CTA GGA TAC TGT AGC TTC TCT AAG TCC AGA 1606

I L N T L L S P A Q L K L H K I F L H Q 489
ATC CTC AAC ACA CTT CTC AGC CCT GCC CAG TTG AAA TTA CAC AAA ATC TTT CTT CAT CAA 1666

D L P L L V L P R Q I S D G L V E I T W 509
GAT TTG CCT CTT TTG GTG CTT CCC CGG CAA ATC TCT GAT GGC CTG GTT GAG ATA ACA TGG 1726

C F P D S D D R K E N P F F Q K P V A L 529
TGT TTT CCT GAT AGC GAT GAT AGA AAG GAA AAC CCC TTT TTC CAA AAG CCT GTT GCT CTG 1786

A N L R G N L E S F W T Q F G F L M E V 549
GCT AAT CTC CGT GGA AAT CTA GAA AGT TTT TGG ACT CAG TTT GGT TTT TTG ATG GAA GTT 1846

S S A V F F F T D C L G E K E W D L L M 569
TCT TCA GCT GTG TTT TTT TTC ACT GAC TGT TTA GGT GAG AAG GAA TGG GAC TTG CTA ATG 1906

F L G E A A I E R C Y F V L S S Q A R E 589
TTT TTA GGA GAG GCT GCC ATT GAA AGA TGC TAC TTT GTT CTC AGT TCC CAA GCC AGG GAG 1966

S E E A Q I F Q R I L N L K P A Q L L F 609
AGT GAA GAG GCT CAA ATT TTT CAG AGG ATA CTG AAC TTG AAG CCA GCA CAG CTA CTG TTT 2026

W E R G D A G D R R K N M E G L Q A A L 629
TGG GAG AGG GGA GAT GCT GGG GAT AGA AGG AAG AAC ATG GAG GGC CTT CAA GCT GCC CTC 2086

Q E V M F S S C L R C V S V E D M A A L 649
CAG GAA GTG ATG TTC TCT TCT TGC CTC AGA TGT GTG TCT GTG GAG GAT ATG GCC GCC CTG 2146

A R E L G I Q V D E D F E N T Q R I Q V 669
GCC AGG GAG CTG GGG ATT CAG GTA GAT GAA GAC TTT GAA AAC ACT CAG AGA ATT CAA GTT 2206

S S G E N M A G T A E G E G Q Q R H S Q 689
TCC TCT GGA GAA AAC ATG GCT GGG ACA GCT GAA GGT GAG GGT CAG CAA AGA CAC AGT CAG 2266

L K S S S K S Q A L M P I Q E P G T Q C 709
CTA AAA AGC TCA TCT AAA AGC CAG GCT CTA ATG CCA ATT CAA GAG CCT GGG ACT CAA TGT 2326

E L S Q N L Q N L Y G T P V F R P V L E 729
GAG CTC AGC CAG AAT CTT CAG AAT CTC TAT GGT ACC CCA GTA TTC AGG CCT GTT CTA GAG 2386

N S W L F P T R I G G N F N H V S L K A 749
AAC TCC TGG CTC TTT CCA ACC AGA ATT GGA GGT AAC TTT AAC CAT GTT TCC TTG AAA GCC 2446

S W V M G R P F G S E Q R P K W F H P L 769
TCC TGG GTT ATG GGC CGC CCC TTT GGG TCA GAG CAG AGG CCT AAG TGG TTC CAT CCT TTG 2506

FIG. 28B



P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTCTATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTGTTTG 3471

TTTGAGACAGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAATGGCAGCATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTATAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTGGGATTACGTGTGTAAGCCACAGTGCCCGAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATGAAAATAATTAAGACTAGAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGACCCAGGGAATGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

FIG. 28C



GCTCCAGAGGTATCTTTGTCAAAAGCTTCTGTTCAATATCAGCCACTGAGCAGATAACCCCTGCTTATTGGTGGTT 4103
AAATCAACTAGCTTCTGCTAATAGCCCCCAATTGCTTGAATGGGAAACTCTCTCATTGGACCCCTTATAGGTAGAAATA 4182
ATGAATTAAACAACCAATAAAATTAATCAATTGGCAATTAATAAAAAAAAAAAAAAAAAAAAAA 4244

FIG. 28D

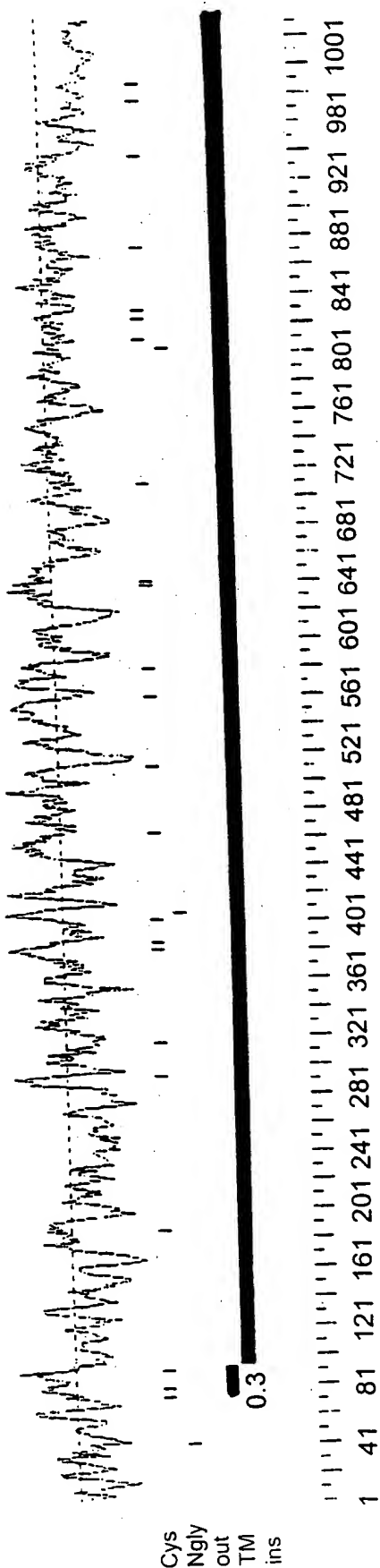


FIG. 29



NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

```
CONSENSUS      *-->maederrllkknrvrliesLgldvLdelldvLlekdvlnlkeeEkik
                +++ + ++ r++l+e+L+ d +Ld L +++++ ++e E
CARD6          5  STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLLISEEEYETLE 48

CONSENSUS      ragakledDKarelvdslqrrgsqafdaifaledTgqsyLAdvLel<--*
                + l + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6          49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92
```

FIG. 30

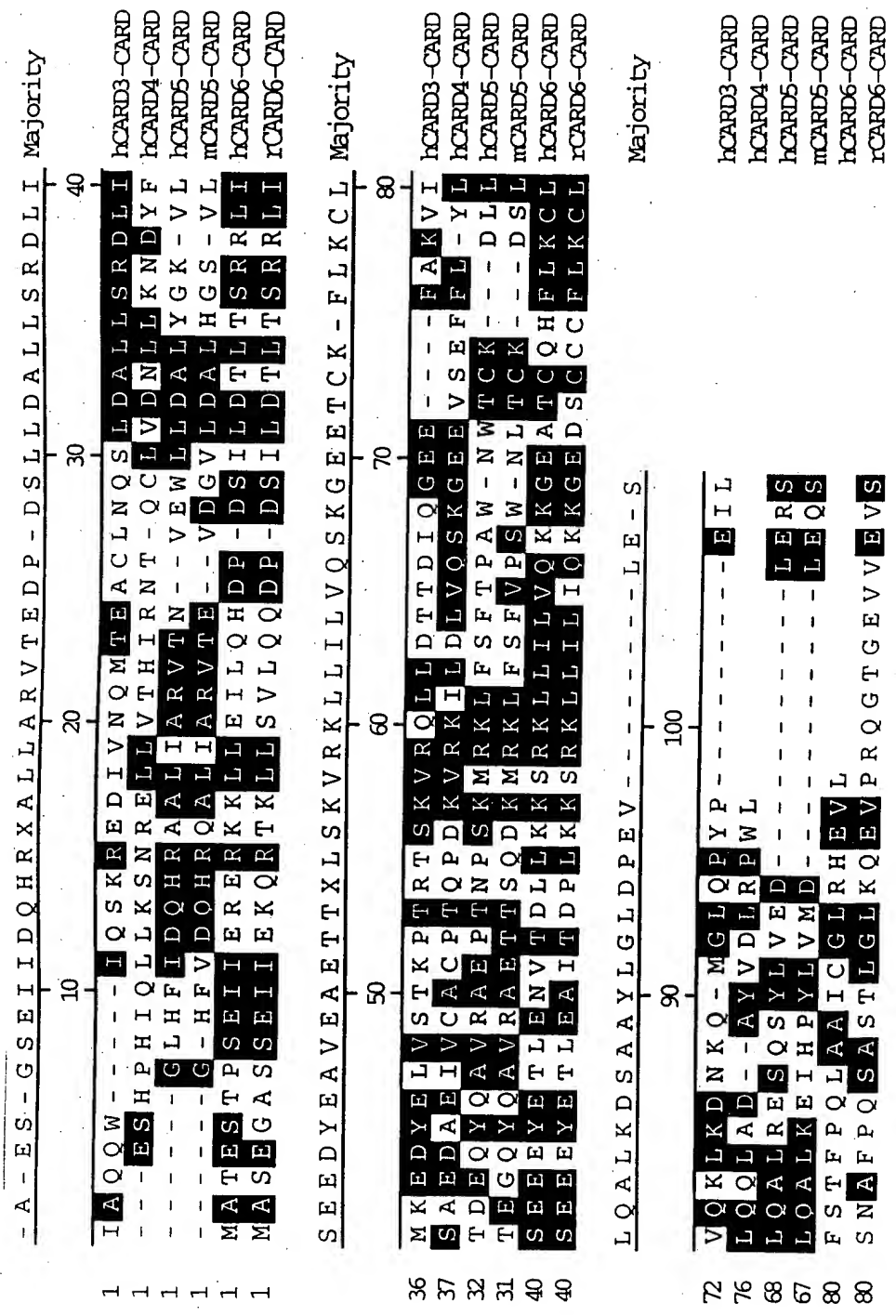


FIG. 31